

On page 66, at the end of line 8, please insert --(SEQ ID NO: 9)--.

At page 65, line 27, after "(Novo Nordisk A/S)", insert --SEQ ID NO:2--.

At page 67, line 21, after "WO 95/26397", insert --(SEQ ID NO:1 of WO 95/26397 is shown in Fig. 8 of the instant application, SEQ ID NO:12)--.

Please delete pages 69-75 (Sequence Listing), insert the substitute Sequence Listing appended herewith (marked as pages 69-89), and re-number the subsequent pages accordingly.

IN THE CLAIMS:

Cancel claims 1-70 without prejudice or disclaimer.

Add new claims 71 and 72 reading as follows:

Sub C1
--71. A method of producing a variant of a parent alpha-amylase having an altered property relative to the parent, wherein the parent alpha-amylase has the sequence of SEQ ID Nos: 2, 4, 6, or 13, or has a sequence at least 70 % homologous to the sequence of SEQ ID Nos: 2, 4, 6, or 13 when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, said method comprising

(a) modelling the parent alpha-amylase on an X-ray crystallographic three-dimensional structure of an alpha-amylase having the sequence of SEQ ID Nos: 2, 4, 6, or 13, or having a sequence at least 70 % homologous to the sequence of SEQ ID Nos: 2, 4, 6, or 13 when homology is determined by the GAP program using default values for GAP penalties, to produce a three-dimensional structure of the parent alpha-amylase;

(b) identifying in the three-dimensional structure obtained in step (a) at least one structural part of the parent wherein an alteration in said structural part is predicted to result in said altered property;

(c) modifying the sequence of a nucleic acid encoding the parent alpha-amylase to produce a nucleic acid encoding a deletion, insertion, or substitution of one or more amino acids at a position corresponding to said structural part; and

(d) expressing the modified nucleic acid to produce the variant alpha-amylase, wherein the variant has alpha-amylase enzymatic activity and has at least one altered property relative to the parent. --

(a) modelling the parent alpha-amylase on an X-ray crystallographic three-dimensional structure of an alpha-amylase having the sequence of SEQ ID Nos: 2, 4, 6, or 13, or having a sequence at least 70% homologous to the sequence of SEQ ID Nos: 2, 4, 6, or 13 when homology is determined by the GAP program using default values for GAP penalties, to produce a three-dimensional structure of the parent alpha-amylase;

(b) comparing the three-dimensional structure obtained in step (a) with a three-dimensional structure of an unrelated alpha-amylase, wherein the unrelated alpha-amylase differs from the parent alpha-amylase in said property;

(c) identifying a structural part of the three-dimensional structure obtained in step (a) which is different from the three-dimensional structure of the unrelated alpha-amylase and which is predicted to be relevant to said property,

(d) modifying the sequence of a nucleic acid encoding the parent alpha-amylase to produce a nucleic acid encoding a deletion, insertion, or substitution of one or more amino acids at a position corresponding to said structural part; and

(e) expressing the modified nucleic acid to produce the variant alpha-amylase, wherein the variant has alpha-amylase activity and has one or more altered properties as compared to the parent alpha-amylase. --

Entry of this amendment is respectfully requested.

In this response, claims 1-70 are cancelled without prejudice and new claims 71 and 72 are added. Support for the new claims can be found in the specification and original claims. For example, the definition of a parent (Termamyl-like) alpha-amylase can be found in the specification at page 5, lines 4-20. The process of modelling a parent alpha-amylase on a three-dimensional structure is described on page 12, lines 7-24; and on page 62, line 4 - page 63, line 5 (Example 1). Production of a variant alpha-amylase by modification

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